Supplemental Figures

Supplementary Figure 1. Top 10 most frequently mutated genes.
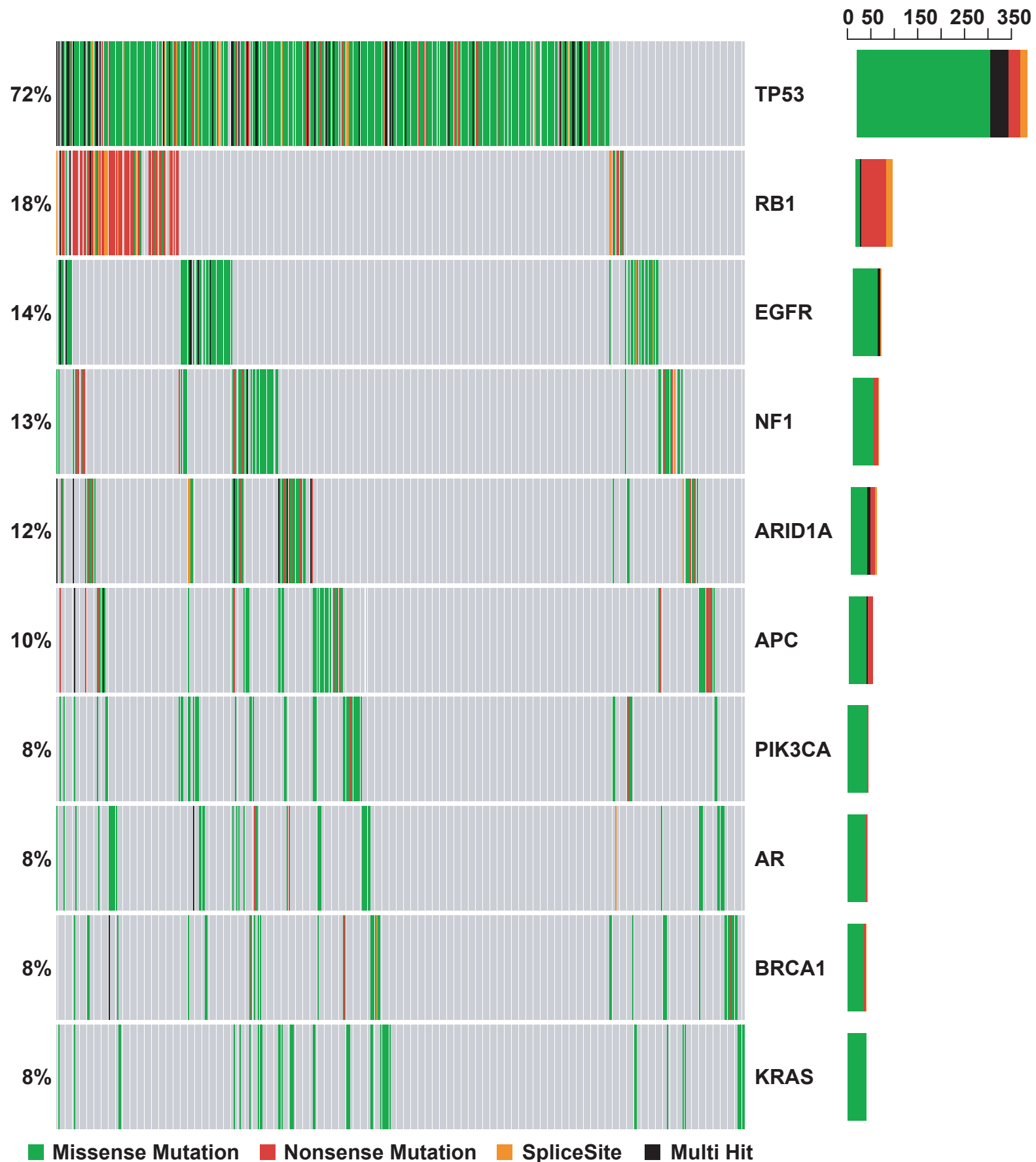
Supplementary Figure 2. Frequency of missense and nonsense mutations in TP53 and RB1 and their distribution across all samples.

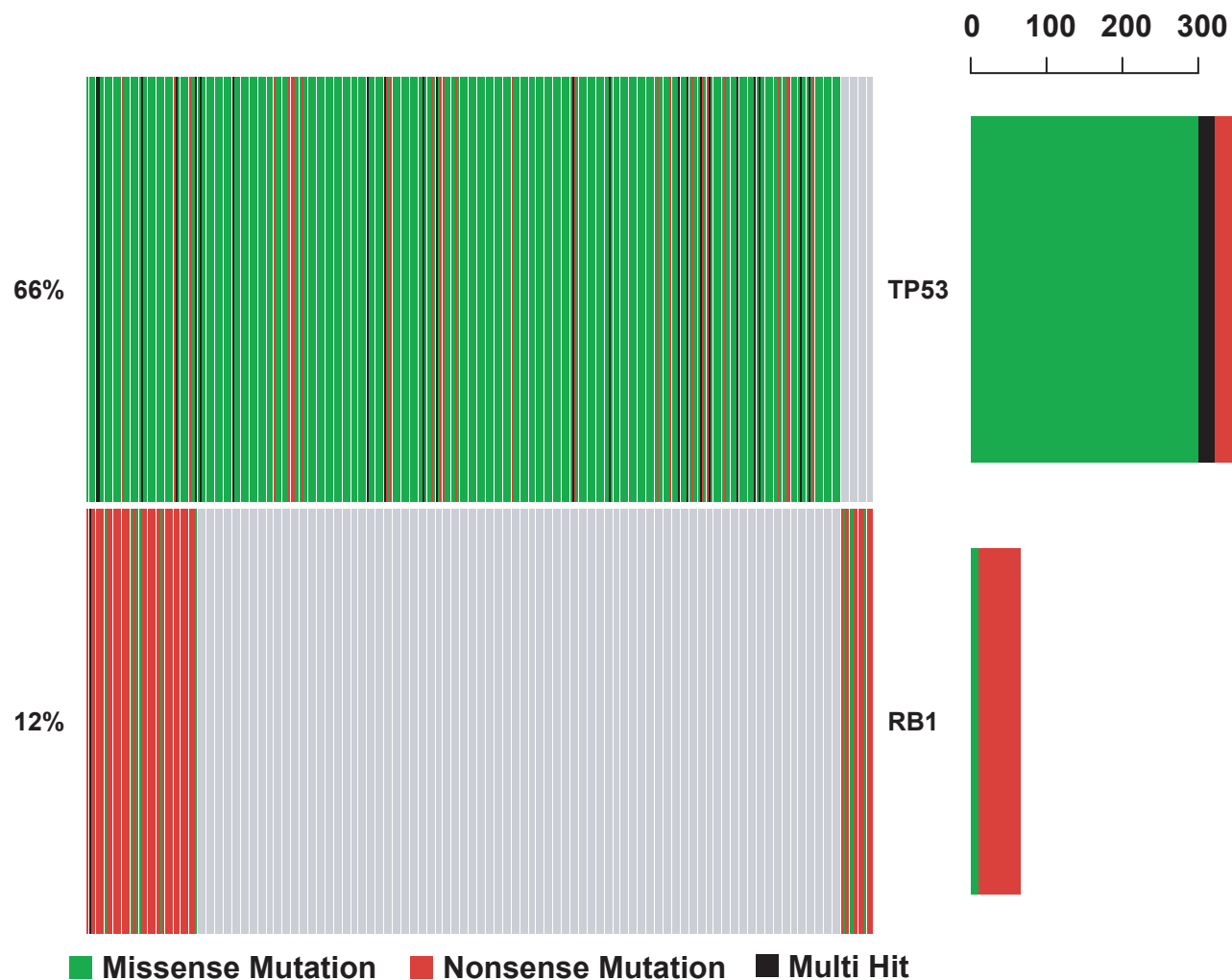**Supplementary Figure 3. The distribution of APC mutations across different domains of the gene.**

Supplementary Figure 4. Amplifications in MYC.

Supplementary Figure 5. TP53 mutations across SCLC samples with multiple mutations.
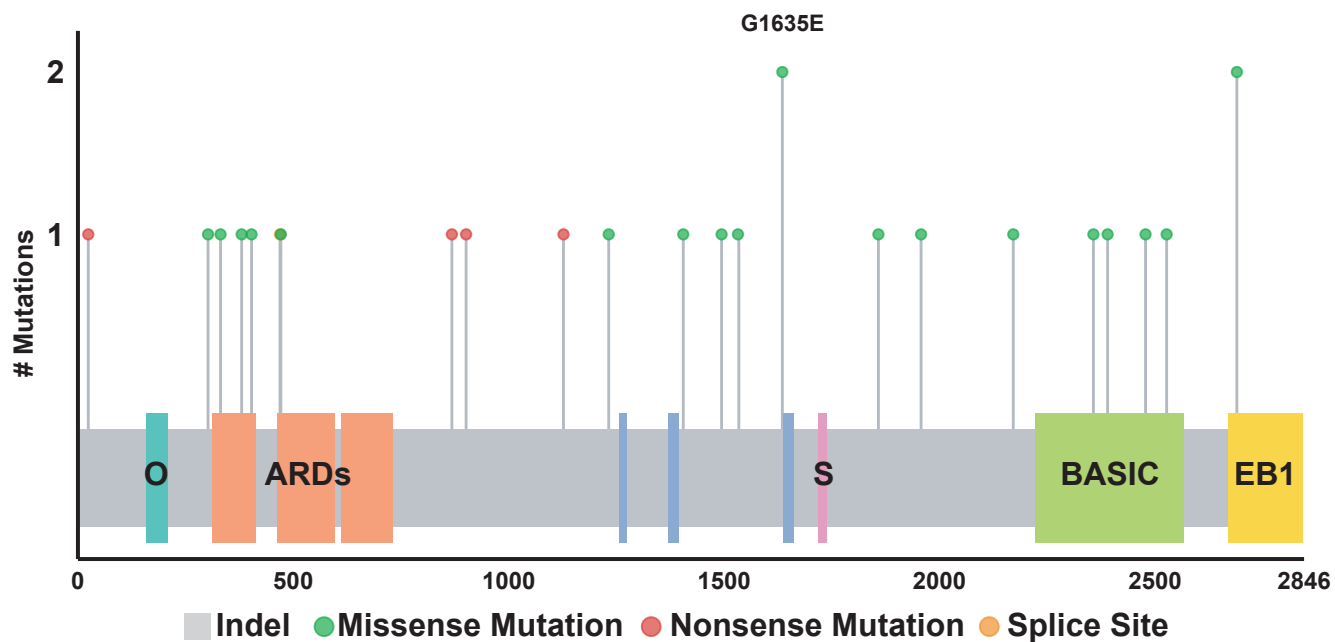
Supplementary Figure 6. Oncoplot demonstrating distribution of the ten most frequently altered genes across samples collected at diagnosis.
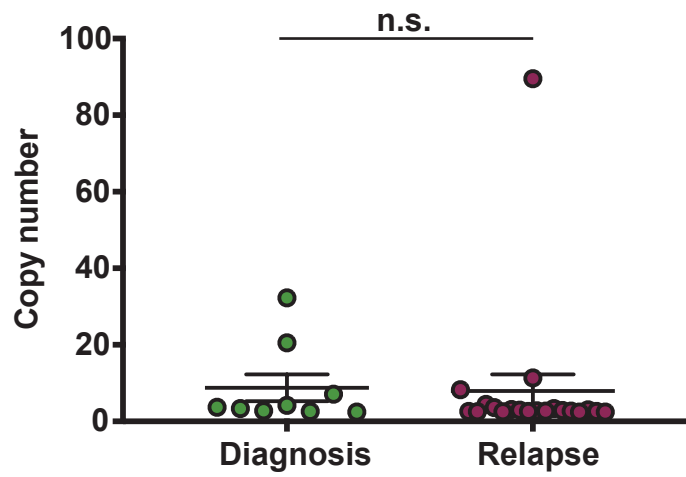
Supplementary Figure 1. Top 10 most frequently mutated genes. Oncoplot demonstrating distribution of the ten most frequently altered genes across all samples. The right barplot represents the frequency of mutations in each gene. Multi Hit = presence of multiple types of mutation in same gene in a given sample. Each column represents an individual patient sample.

Supplementary Figure 2. Frequency of missense and nonsense mutations in TP53 and RB1 and their distribution across all samples. The right barplot represents the frequency of mutations in each gene. Multi-Hit = presence of multiple types of mutation in same gene in a given sample. Each column represents an individual patient sample.
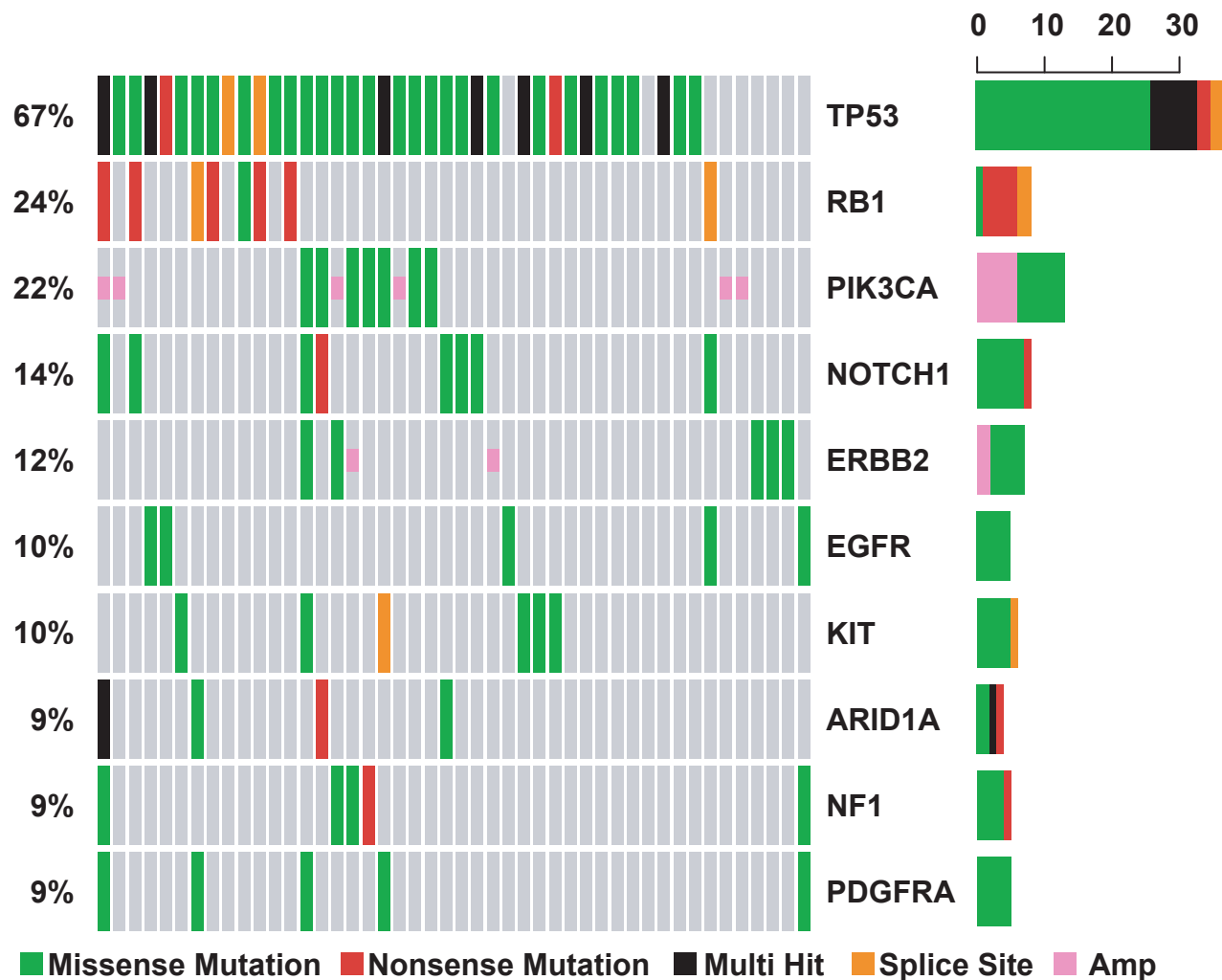
Supplementary Figure 3. The distribution of APC mutations across different domains of the gene. O = oligomerization. ARDs = Armadillo Repeat Domains. S = Ser-Ala-Met-Pro (SAMP) motif. EB1 = EB1 binding domain.

Supplementary Figure 4. Amplifications in MYC. The distribution of the number of copies of MYC across diagnosis and relapse samples in which they are amplified. Error bars represent Mean ± SEM. n.s = not significant.
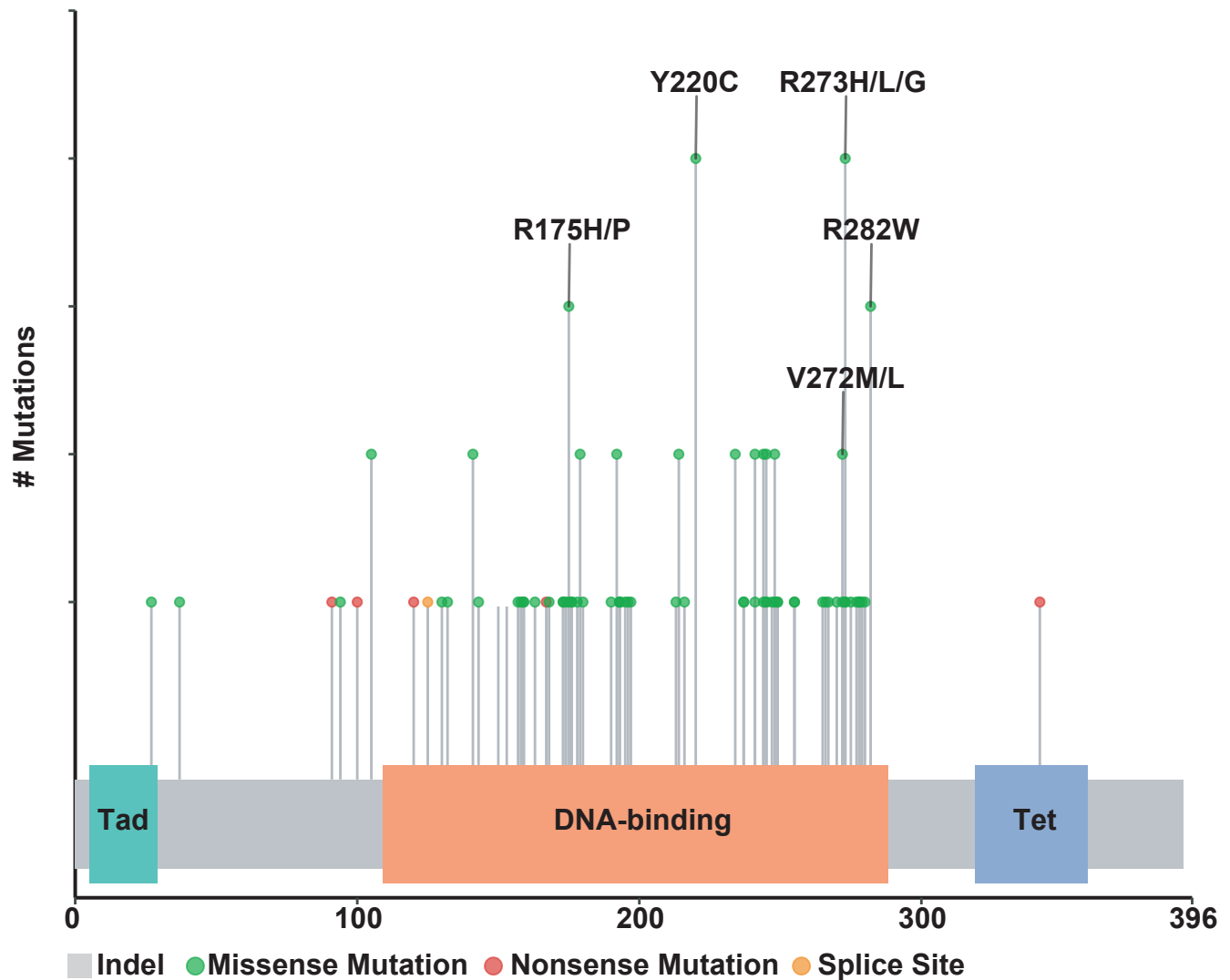
Supplementary Figure 5. TP53 mutations across SCLC samples with multiple mutations.
Demonstrates mutation pattern of mutations in TP53 that were shed at lower allelic frequecies in samples showing multiple mutations. Tad = Transactivating domain. Tet = Tetrameriization domain.

Supplementary Figure 6. Oncoplot demonstrating distribution of the ten most frequently altered genes across samples collected at diagnosis. Amp = amplification, Multi-Hit = presence of multiple types of mutation in same gene in a given sample. Each column represents an individual patient sample. The right barplot represents the frequency of mutations in each gene.